## RECEIVED

SEQUENCE LISTING

AUG 2 2 2001

**TECH CENTER 1600/2900** 

<110> COLLESI, Chiara

CASELLI, Gianfranco COMOGLIO, Paolo

RECOMBINANT PROTEINS DERIVED FROM HGF AND MSP

<130> 0471-0162P

<140> US 09/600,991 <141> 2000-09-15

<160> 22

<170> PatentIn version 3.1

<210> 1 <211> 1725 <212> DNA

<213> Artificial Sequence

<220>

<223> Magic F-1 DNA coding sequence

<400> 1

/400/ I						
atgtgggtga	ccaaactcct	gccagccctg	ctgctgcagc	atgtcctcct	gcatctcctc	60
ctgctcccca	tcgccatccc	ctatgcagag	ggacaaagga	aaagaagaaa	tacaattcat	120
gaattcaaaa	aatcagcaaa	gactacccta	atcaaaatag	atccagcact	gaagataaaa	180
accaaaaaag	tgaatactgc	agaccaatgt	gctaatagat	gtactaggaa	taaaggactt	240
ccattcactt	gcaaggcttt	tgtttttgat	aaagcaagaa	aacaatgcct	ctggttcccc	300
ttcaatagca	tgtcaagtgg	agtgaaaaaa	gaatttggcc	atgaatttga	cctctatgaa	360
aacaaagact	acattagaaa	ctgcatcatt	ggtaaaggac	gcagctacaa	gggaacagta	420
tctatcacta	agagtggcat	caaatgtcag	ccctggagtt	ccatgatacc	acacgaacac	480
agctatcggg	gtaaagacct	acaggaaaac	tactgtcgaa	atcctcgagg	ggaagaaggg	540
ggaccctggt	gtttcacaag	caatccagag	gtacgctacg	aagtctgtga	cattcctcag	600
tgttcagaag	ttgaatgcat	gacctgcaat	ggggagagtt	atcgaggtct	catggatcat	660
acagaatcag	gcaagatttg	tcagcgctgg	gatcatcaga	caccacaccg	gcacaaattc	720
ttgcctgaaa	gatatcccga	caagggcttt	gatgataatt	attgccgcaa	tcccgatggc	780
cagccgaggc	catggtgcta	tactcttgac	cctcacaccc	gctgggagta	ctgtgcaatt	840
aaaacatgcg	ctgacaaagc	ttcgggcggt	ggcggttctg	gtggcggtgg	ctccggcggt	900
ggcggttctc	tagagggaca	aaggaaaaga	agaaatacaa	ttcatgaatt	caaaaaatca	960
gcaaagacta	ccctaatcaa	aatagatcca	gcactgaaga	taaaaaccaa	aaaagtgaat	1020
actgcagacc	aatgtgctaa	tagatgtact	aggaataaag	gacttccatt	cacttgcaag	1080
gcttttgttt	ttgataaagc	aagaaaacaa	tgcctctggt	tccccttcaa	tagcatgtca	1140
agtggagtga	aaaaagaatt	tggccatgaa	tttgacctct	atgaaaacaa	agactacatt	1200
agaaactgca	tcattggtaa	aggacgcagc	tacaagggaa	cagtatctat	cactaagagt	1260
ggcatcaaat	gtcagccctg	gagttccatg	ataccacacg	aacacagcta	tcggggtaaa	1320
gacctacagg	aaaactactg	tcgaaatcct	cgaggggaag	aagggggacc	ctggtgtttc	1380
acaagcaatc	cagaggtacg	ctacgaagtc	tgtgacattc	ctcagtgttc	agaagttgaa	1440
tgcatgacct	gcaatgggga	gagttatcga	ggtctcatgg	atcatacaga	atcaggcaag	1500
atttgtcagc	gctgggatca	tcagacacca	caccggcaca	aattcttgcc	tgaaagatat	1560
cccgacaagg	gctttgatga	taattattgc	cgcaatcccg	atggccagcc	gaggccatgg	1620
tgctatactc	ttgaccctca	cacccgctgg	gagtactgtg	caattaaaac	atgcgctgac	1680
aaagctgacg	acgacgacaa	acaccaccac	caccaccacc	actag		1725





<210> 2 <211> 574 <212> PRT <213> Artificial Sequence <220> <223> Magic F-1 recombinant protein obtained combining hairpin loop and kringle domains of human HGF and MSP <400> Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu Leu His Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr 40 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu 70 80 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe 105 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys 115 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys 135 140 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His 145 150 155 Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg 165 170 Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg 185 Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr 195 200 205 Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe

240

235

230

Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg 245 Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His 265 Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Lys Ala Ser 280 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu 290 Glu Gly Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser 310 315 Ala Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr 330 Lys Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn 340 Lys Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg 360 Lys Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys 380 375 Lys Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile 395 390 385 Arg Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser 410 Ile Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro 420 His Glu His Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro 455 Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu 465 Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr 490 Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg 505 His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn 520 515 Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu 535 530

3 42

```
Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp
545
                    550
Lys Ala Asp Asp Asp Lys His His His His His His
                565
                                    570
<210>
       3
      1692
<211>
<212>
      DNA
<213> Artificial Sequence
<220>
<223>
       Metron F-1 DNA coding sequence
<400>
atggggtggc teccaetect getgettetg acteaatget taggggteee tgggeagege
                                                                       60
tegecattga atgaetteea agtgeteegg ggeacagage tacageacet getacatgeg
                                                                      120
gtggtgcccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc tggtcgctgt
                                                                      180
gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg ttgccaactg
                                                                      240
ctgccatgga ctcaacactc gccccacacg aggctgcggc gttctgggcg ctgtgacctc
                                                                      300
                                                                      360
ttccagaaga aagactacgt acggacctgc atcatgaaca atggggttgg gtaccggggc
accatggcca cgaccgtggg tggcctgccc tgccaggctt ggagccacaa gttcccgaat
                                                                      420
gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg ccgtaaccct
                                                                      480
gatggcgacc ccggaggtcc ttggtgctac acaacagacc ctgctgtgcg cttccaqaqc
                                                                      540
                                                                      600
tgcqqcatca aatcctqccq qqaqqccqcq tqtqtctqqt qcaatqqcqa ggaataccgc
ggcgcggtag accgcacgga gtcagggcgc gagtgccagc gctgggatct tcagcacccg
                                                                      660
                                                                      720
caccagcacc ccttcgagcc gggcaagttc ctcgaccaag gtctggacga caactattgc
                                                                      780
cqqaatcctq acqqctccqa qcqqccatqq tqctacacta cqqatccqca qatcqaqcqa
gagttctgtg acctcccccg ctgcgggtcc gaggcacagc cccgcctcga gggcggtggc
                                                                      840
qqttctqqtq qcqqtqqctc cqqcqqtqqc qqttctctag agggacaaag gaaaagaaga
                                                                      900
                                                                      960
aatacaatto atgaattoaa aaaatoagoa aagaotacoo taatoaaaat agatooagoa
ctgaagataa aaaccaaaaa agtgaatact gcagaccaat gtgctaatag atgtactagg
                                                                     1020
aataaaggac ttccattcac ttgcaaggct tttgtttttg ataaagcaag aaaacaatgc
                                                                     1080
ctctgqttcc ccttcaatag catgtcaagt ggagtgaaaa aagaatttgg ccatgaattt
                                                                     1140
qacctctatq aaaacaaaqa ctacattaqa aactqcatca ttqqtaaaqg acgcaqctac
                                                                     1200
aagggaacag tatctatcac taagagtggc atcaaatgtc agccctggag ttccatgata
                                                                     1260
ccacacqaac acagctatcg gggtaaagac ctacaggaaa actactgtcg aaatcctcga
                                                                     1320
qqqqaaqaag qqqqaccctq qtqtttcaca aqcaatccag aggtacgcta cgaagtctgt
                                                                     1380
qacattcctc agtgttcaga agttgaatgc atgacctgca atggggagag ttatcgaggt
                                                                     1440
                                                                     1500
ctcatggatc atacagaatc aggcaagatt tgtcagcgct gggatcatca gacaccacac
cggcacaaat tettgcetga aagatateee gacaaggget ttgatgataa ttattgeege
                                                                     1560
aatcccqatq qccaqccqaq qccatqqtqc tatactcttq accctcacac ccgctqgqaq
                                                                     1620
tactqtqcaa ttaaaacatq cqctqacaaa qctqacqacq acgacaaaca ccaccaccac
                                                                     1680
                                                                     1692
caccaccact aq
<210>
       4
<211>
       563
<212>
       PRT
<213>
      Artificial Sequence
<220>
       Metron F-1 recombinant protein obtained combining hairpin loop and
```



kringle domains of human HGF and MSP

<223>

## <400> 4

Met Gly Trp Leu Pro Leu Leu Leu Leu Thr Gln Cys Leu Gly Val 1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr 20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu 35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met 50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu 65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly 85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met 100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly 115 120 125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr 130 135 140

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro 145 150 155 . 160

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val 165 170 175

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val 180 185 190

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser 195 200 205

Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro 210 215 220

Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys 225 230 235 240

Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro 245 250 255

Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala 260 265 270

Gln Pro Arg Leu Glu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly 275 280 285

Gly Gly Gly Ser Leu Glu Gly Gln Arg Lys Arg Arg Asn Thr Ile His





290 295 300

Glu Phe Lys Lys Ser Ala Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala 315 310 Leu Lys Ile Lys Thr Lys Lys Val Asn Thr Ala Asp Gln Cys Ala Asn 330 Arg Cys Thr Arg Asn Lys Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys Leu Trp Phe Pro Phe Asn Ser Met 360 Ser Ser Gly Val Lys Lys Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr 390 Lys Gly Thr Val Ser Ile Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp 410 Ser Ser Met Ile Pro His Glu His Ser Tyr Arg Gly Lys Asp Leu Gln 420 Glu Asn Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly 470 Leu Met Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His 490 Gln Thr Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys 500 510 Gly Phe Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile

Lys Thr Cys Ala Asp Lys Ala Asp Asp Asp Lys His His His His

His His His

<210> 5 <211> 36 <212> DNA

45

B

<213>	Artificial Sequence	
<220> <223>	Oligonucleotide primer targeted to human MSP cDNA	
<400> cgcgcg	5 gaat tecaceatgg ggtggetece acteet	36
<210><211><211><212><213>	36	
<220> <223>	Oligonucleotide primer targeted to human MSP cDNA	
<400> cgcgcg	6 ctcg aggcggggct gtgcctcgga cccgca	36
<210> <211> <212> <213>		
<220> <223>	Oligonucleotide primer targeted to human HGF cDNA	
<400> cgcgcg	7 tcta gagggacaaa ggaaaagaag aaatac	36
<210><211><211><212><213>	36	
<220> <223>	Oligonucleotide primer targeted to human HGF cDNA	
<400> cgcgcg	8 aagc tttgtcagcg catgttttaa ttgcac	36
<210><211><211><212><213>		
<220> <223>	Oligonucleotide primer used to synthesize the Metron Factor-1 linker sequence	
<400> tcgagg	9 gcgg tggcggttct ggtggcggtg gctccggcgg tggcggttct	50

L

<210> <211> <212> <213>	10 50 DNA Artificial Sequence
<220> <223>	Oligonucleotide primer used to synthesize the Metron Factor-1 linker sequence
<400> ctagaga	10 aacc gccaccgccg gagccaccgc caccagaacc gccaccgccc 50
<210> <211> <212> <213>	11 50 DNA Artificial Sequence
<220> <223>	Oligonucleotide primer used to insert the tag sequence in Metron Factor-1
<400> agctga	11 cgac gacgacaaac accaccacca ccaccaccac tagggtcgac 50
	12 50 DNA Artificial Sequence
<220> <223>	Oligonucleotide primer used to insert the tag sequence in Metron Factor-1
<400> agctgto	12 cgac cctagtggtg gtggtggtgg tggtgtttgt cgtcgtcgtc 50
<210><211><212><212><213>	13 36 DNA Artificial Sequence
<220> <223>	Oligonucleotide primer targeted to human HGF cDNA
<400> cgcgcg	13 ggat cegecageeg etecageage accatg 36
<210><211><211><212><213>	14 36 DNA Artificial Sequence

	Oligonucleotide primer targeted to human HGF cDNA	
<400>	14 agc tttgtcagcg catgttttaa ttgcac	36
<210>		
<211>		
<212> <213>	Artificial Sequence	
	•	
<220> <223>	Oligonucleotide primer used to synthesize the Magic Factor-1	
<b>\</b> 2237	linker sequence	
.400>		
<400>	15 ggge ggtggeggtt etggtggegg tggeteegge ggtggeggtt et	52
5 :	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
<210>	16	
<211>		
<212>	DNA .	
<213>	Artificial Sequence	
<220>		
<223>	Oligonucleotide primer used to synthesize the Magic Factor-1	
	linker sequence	
<400>		
ctagaga	aacc gccaccgccg gagccaccgc caccagaacc gccaccgccc ga	52
.<210>		
<211>		
<212>	DNA	
<212>		
<212> <213> <220>	DNA Homo sapiens	
<212> <213> <220> <221>	DNA Homo sapiens . CDS	
<212> <213> <220>	DNA Homo sapiens	
<212> <213> <220> <221> <222>	DNA Homo sapiens . CDS	
<212> <213> <220> <221> <222>	DNA Homo sapiens  CDS (1)(2172)	
<212><213><220><221><222><223><400>atg tgg	DNA Homo sapiens  CDS (1)(2172)  17 g gtg acc aaa ctc ctg cca gcc ctg ctg ctg cag cat gtc ctc	48
<212><213> 220 221 221 222 223 400 <atg met="" td="" tgg="" tri<=""><td>DNA Homo sapiens  CDS (1)(2172)  17 g gtg acc aaa ctc ctg cca gcc ctg ctg cag cat gtc ctc Val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu</td><td>48</td></atg>	DNA Homo sapiens  CDS (1)(2172)  17 g gtg acc aaa ctc ctg cca gcc ctg ctg cag cat gtc ctc Val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu	48
<212><213><220><221><222><223><400>atg tgg	DNA Homo sapiens  CDS (1)(2172)  17 g gtg acc aaa ctc ctg cca gcc ctg ctg ctg cag cat gtc ctc	48
<212><213> 220 221 222 223 400 <atg 1<="" met="" p="" tgg="" tri=""></atg>	DNA Homo sapiens  CDS (1)(2172)  17 g gtg acc aaa ctc ctg cca gcc ctg ctg ctg cag cat gtc ctc val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu 5 c ctc ctc ctg ctc ccc atc gcc atc ccc tat gca gag gga caa	48
<212><213> 220 221 222 223 400 <atg 1<="" met="" p="" tgg="" tri=""></atg>	DNA Homo sapiens  CDS (1)(2172)  17 g gtg acc aaa ctc ctg cca gcc ctg ctg ctg cag cat gtc ctc val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu 5 10 15  c ctc ctc ctg ctc ccc atc gcc atc ccc tat gca gag gga caa s Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln	
<212><213> 220 221 222 223 400 <atg 1<="" met="" p="" tgg="" tri=""></atg>	DNA Homo sapiens  CDS (1)(2172)  17 g gtg acc aaa ctc ctg cca gcc ctg ctg ctg cag cat gtc ctc val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu 5 c ctc ctc ctg ctc ccc atc gcc atc ccc tat gca gag gga caa	
<212><213> 223 220 221 222 223 400 <atg a="" tgg<="">det Trictg catLeu His</atg>	DNA Homo sapiens  CDS (1)(2172)  17 g gtg acc aaa ctc ctg cca gcc ctg ctg ctg cag cat gtc ctc val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu 5 10 15  c ctc ctc ctg ctc ccc atc gcc atc ccc tat gca gag gga caa s Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln	





	cta Leu 50				-			-								192	
	act Thr	-	_		-	-		_	_							240	
	ttc Phe															288	
	tgg Trp					_	_		_							336	
	cat His															384	
	att Ile 130				_	_		_			_				_	432	
	ggc Gly															480	
	tat Tyr															528	
	gaa Glu															576	
	gaa Glu	_	_	-			-	-		_	-	-	_	_		624	
_	aat Asn 210			_												672	
	att Ile															720	
_	cct Pro	-	_			-	_			_	_					768	
	ccc Pro	-		_	_											816	
acc	cgc	tgg	gag	tac	tgt	gca	att	aaa	aca	tgc	gct	gac	aat	act	atg	864	





Thr	Arg	Trp 275	Glu	Tyr	Cys	Ala	Ile 280	Lys	Thr	Cys	Ala	Asp. 285	Asn	Thr	Met	
	gac Asp 290		_	_		_	_			_	_					912
	gaa Glu						_									960
_	cag Gln	_		_		_					-	_	_			1008
	aat Asn															1056
	ggg															1104
-	ggc Gly 370		_						-	-						1152
_	tgt Cys		_							_						1200
	aga Arg					_		_		-	-		_	-	-	1248
	cat His															1296
	tac Tyr															1344
_	gga Gly 450							-		_				_	-	1392
	ggt Gly															1440
	tgt Cys															1488
_	aca Thr					_	_	_								1536





	500	505		510	
				et ctt act gca al Leu Thr Ala 525	
	_		-	aa gct tgg ctt Lu Ala Trp Leu 10	
-				gc aaa cag gtt /s Lys Gln Val	
				ca gat ctg gtt er Asp Leu Val 575	
			eu Asp Asp Ph	et gtt agt acg ne Val Ser Thr 590	
				ag acc agt tgc ys Thr Ser Cys 605	
				at gat ggc cta yr Asp Gly Leu 20	
				aa tgc agc cag ys Cys Ser Gln	
				ta tgt gct ggg le Cys Ala Gly 655	
			lu Gly Asp Ty	at ggt ggc cca yr Gly Gly Pro 670	
				gt gtc att gtt ly Val Ile Val 685	
			g Pro Gly Il	tt ttt gtc cga le Phe Val Arg 00	
				ta aca tat aag eu Thr Tyr Lys	
cca cag tca Pro Gln Ser	-				2172





<210> 18 <211> 723

<212> PRT

<213> Homo sapiens

<400> 18

Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu  $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$ 

Leu His Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
20 25 30

Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr 35 40 45

Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val 50 60

Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu 65 70 75 80

Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys 85 90 95

Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe 100 105 110

Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys 115 120 125

Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys 130 135 140

Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His 145 150 155 160

Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg 165 170 175

Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg 180 185 190

Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr 195 200 205

Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly 210 215 220

Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe 225 230 235 240

Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg 245 250 255





Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His 265 Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr Met 280 Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly Gln 295 Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile Pro 310 315 Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr Pro 330 335 325 Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn Pro 345 Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile Arg 360 Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly Gln 375 Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser Gln 395 Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu Asp 410 Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn Glu 425 420 Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys Tyr 440 Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg Cys 450 Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val Ile 470 Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile Pro Thr 490 Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys His 500 Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala Arg 520 Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly 535



560

555

Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu

550

Asn Val Ser Gln Leu Val Tyr Gly 565	Pro Glu Gly 570		Val Leu 575
Met Lys Leu Ala Arg Pro Ala Va 580	Leu Asp Asp 585	Phe Val Ser T	Chr Ile
Asp Leu Pro Asn Tyr Gly Cys Th: 595 600		Lys Thr Ser 0	Cys Ser
Val Tyr Gly Trp Gly Tyr Thr Gly 610 615	/ Leu Ile Asn	Tyr Asp Gly I 620	Seu Leu
Arg Val Ala His Leu Tyr Ile Met 625 630	Gly Asn Glu 635	Lys Cys Ser (	Gln His 640
His Arg Gly Lys Val Thr Leu Asa 645	Glu Ser Glu 650		Gly Ala 555
Glu Lys Ile Gly Ser Gly Pro Cy: 660	Glu Gly Asp 665	Tyr Gly Gly 670	Pro Leu
Val Cys Glu Gln His Lys Met Arc 675 680		Gly Val Ile V 685	/al Pro
Gly Arg Gly Cys Ala Ile Pro Ass 690 695	n Arg Pro Gly	Ile Phe Val A	Arg Val
Ala Tyr Tyr Ala Lys Trp Ile Hi: 705 710	S Lys Ile Ile 715	Leu Thr Tyr I	Lys Val 720
Pro Gln Ser			
<210> 19 <211> 2136 <212> DNA <213> Homo sapiens			
<220> <221> CDS <222> (1)(2136) <223>			
<400> 19 atg ggg tgg ctc cca ctc ctg ctc Met Gly Trp Leu Pro Leu Leu Leu 1 5		Gln Cys Leu (	
cct ggg cag cgc tcg cca ttg aa Pro Gly Gln Arg Ser Pro Leu As 20	_		
gag cta cag cac ctg cta cat gc Glu Leu Gln His Leu Leu His Al 35 40			

	gtg Val 50															192
	tgc Cys															240
_	cca Pro					_			_		_		-			288
_	tgt Cys	_			_	-		_		-			-		_	336
	aat Asn															384
_	ccc Pro 130	_	_	_		_		_		_		_		_		432
_	ccc Pro						_	_				_	_			480
	ggc Gly															528
_	ttc Phe	_	_	_					_			_		_	_	576
	tgc Cys															624
222	cgc Arg 210		_	_	_		_		_		_		_			672
	gag Glu															720
	aat Asn		-							-			_	_	_	768
	atc Ile		_			_				_	_				-	816





_	ccc	-			-			-	_	_		_				864
	ggc Gly 290															912
	cgt Arg															960
	tac Tyr															1008
	tca Ser					-			-				_			1056
	ttt Phe															1104
_	tgc Cys 370				-			-		-		_	-	_	_	1152
	cgc Arg															1200
_	ccg Pro	-		_				_	_		_		_			1248
	ttc Phe	-				_		_	_							1296
	atg Met															1344
	gat Asp 450															1392
	gag Glu	-	_		_			_		_	-	_		_		1440
	ctg Leu														gtc Val	1488
ago	: ttg	cgg	aat	cgg	cag	ggc	cag	cat	ttc	tgc	ggg	ggg	tct	cta	gtg	1536

Ser	Leu	Arg	Asn 500	Arg	Gln	Gly	Gln	His 505	Phe	Cys	Gly	Gly	Ser 510	Leu	Val	
_		_			ctg Leu		_		_	_				_		1584
					tat Tyr											1632
	_				cca Pro 550	-		-		-		-	_	_	_	1680
					ggc Gly											1728
			_		cag Gln	_		_	_		_	_				1776
					cca Pro			_	_			-				1824
				_	ggt Gly		_		-				-		_	1872
	-				cag Gln 630		_			-		_		-		1920
		-		_	tgc Cys				_	_	_				-	1968
					ggg Gly											2016
					att Ile											2064
					ttc Phe											2112
	_	_	_	_	ctg Leu 710		tag									2136

<210> 20



<211> 711

<212> PRT

<213> Homo sapiens

<400> 20

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val 1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr 20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met 50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu 65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly 85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met 100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly 115 120 125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr 130 135 140

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro 145 150 155 160

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val 165 170 175

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val 180 185 190

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
195 200 205

Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro 210 215 220

Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys 225 230 235 240

Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro 245 250 255

Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala 260 265 270





Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly 280 Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Ala Gly Val Pro Cys Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu 310 315 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp 330 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala 340 345 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln 360 Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys 375 Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His 385 390 Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu 410 Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr 430 Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys 435 Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln 455 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser 465 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val 490 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His 515 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn 535 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met 555 550 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg

59

B

570

Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu 585 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly 600 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Phe Leu 615 620 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val 630 635 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala 655 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser 680 685 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile His Lys Val Met Arg Leu Gly 705 <210> 21 <211> 1709 <212> DNA <213> Artificial Sequence <220> <223> Metron F-1 <400> 21 gaattccacc atggggtggc tcccactcct gctgcttctg actcaatgct taggggtccc 60 tgggcagcgc tcgccattga atgacttcca agtgctccgg ggcacagagc tacagcacct 120 gctacatgcg gtggtgcccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc 180 tggtcgctgt gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg 240 ttgccaactg ctgccatgga ctcaacactc gccccacacg aggctgcggc gttctgggcg 300 ctgtgacctc ttccagaaga aagactacgt acggacctgc atcatgaaca atggggttgg 360 qtaccqqqqc accatqqcca cqaccqtqqq tqqcctqccc tqccaqqctt qqaqccacaa 420 gttcccqaat gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg 480 ccqtaaccct gatgqcgacc ccqqaqqtcc ttqqtqctac acaacaqacc ctqctqtqcq 540 cttccagage tgeggcatca aatcetgeeg ggaggeegeg tgtgtctggt geaatggega 600 ggaataccgc ggcgcggtag accgcacgga gtcagggcgc gagtgccagc gctgggatct 660 tcagcacccg caccagcacc ccttcgagcc gggcaagttc ctcgaccaag gtctggacga 720 caactattgc cggaatcctg acggctccga gcggccatgg tgctacacta cggatccgca 780 gategagega gagttetgtg aceteceeeg etgegggtee gaggeaeage eeegeetega 840 gggcggtggc ggttctggtg gcggtggctc cggcggtggc ggttctctag agggacaaag 900 qaaaaqaaqa aatacaattc atgaattcaa aaaatcagca aagactaccc taatcaaaat 960 agatecagea etgaagataa aaaccaaaaa agtgaataet geagaccaat gtgetaatag 1020 atgtactagg aataaaggac ttccattcac ttgcaaggct tttgtttttg ataaagcaag 1080 aaaacaatgc ctctggttcc ccttcaatag catgtcaagt ggagtgaaaa aagaatttgg 1140 ccatqaattt qacctctatq aaaacaaaqa ctacattaqa aactqcatca ttqqtaaaqq 1200





acgcagetac aagggaacag tatetateac taagagtggc ateaaatgte agecetggag ttecatgata ceacacgaac acagetateg gggtaaagac etacaggaaa actactgteg aaateetega ggggaacaetg gtgttteaca ageaateeag aggtaegeta egaagtetgt gacatteete agtgtteaga agttgaatge atgaeetgea atggggagag ttategaggt eteatggate atacagaate aggeaagatt tgteageget gggateatea gacaceacae eggeacaaat tettgeetga aagatateee gacaaggget ttgatgataa ttattgeege aateeegatg geeageegag geeatggtge tataeetettg aeceteacae eegetgggag taetgtgeaa ttaaaacatg egetgacaaa getgaegaeg aegacaaacae eegeegaege caccaccae eaceaceae agggtegae	1260 1320 1380 1440 1500 1560 1620 1680 1709
<210> 22	
<211> 1759	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Magic F-1	
<400> 22	60
ggatccgcca gcccgtccag cagcaccatg tgggtgacca aactcctgcc agccctgctg	60
ctgcagcatg tcctcctgca tctcctcctg ctccccatcg ccatccccta tgcagaggga	120 180
caaaggaaaa gaagaaatac aattcatgaa ttcaaaaaat cagcaaagac taccctaatc aaaatagatc cagcactgaa gataaaaacc aaaaaagtga atactgcaga ccaatgtgct	240
aatagatgta ctaggaataa aggacttcca ttcacttgca aggcttttgt ttttgataaa	300
gcaagaaaac aatgcctctg gttccccttc aatagcatgt caagtggagt gaaaaaagaa	360
tttggccatg aatttgacct ctatgaaaac aaagactaca ttagaaactg catcattggt	420
aaaggacgca gctacaaggg aacagtatct atcactaaga gtggcatcaa atgtcagccc	480
tggagttcca tgataccaca cgaacacagc tatcggggta aagacctaca ggaaaactac	540
tgtcgaaatc ctcgagggga agaaggggga ccctggtgtt tcacaagcaa tccagaggta	600
cgctacgaag tctgtgacat tcctcagtgt tcagaagttg aatgcatgac ctgcaatggg	660
gagagttatc gaggtctcat ggatcataca gaatcaggca agatttgtca gcgctgggat	720
catcagacac cacaccggca caaattettg cetgaaagat atecegacaa gggetttgat	780
gataattatt gccgcaatcc cgatggccag ccgaggccat ggtgctatac tcttgaccct	840
cacacceget gggagtactg tgcaattaaa acatgegetg acaaagette gggeggtgge	900
ggttctggtg gcggtggctc cggcggtggc ggttctctag agggacaaag gaaaagaaga	960
aatacaatto atgaattoaa aaaatcagca aagactacco taatcaaaat agatccagca	1020
ctgaagataa aaaccaaaaa agtgaatact gcagaccaat gtgctaatag atgtactagg	1080
aataaaggac ttccattcac ttgcaaggct tttgtttttg ataaagcaag aaaacaatgc	1140
ctctggttcc ccttcaatag catgtcaagt ggagtgaaaa aagaatttgg ccatgaattt	1200
gacctctatg aaaacaaaga ctacattaga aactgcatca ttggtaaagg acgcagctac	1260
aagggaacag tatctatcac taagagtggc atcaaatgtc agccctggag ttccatgata	1320
ccacacgaac acagctatcg gggtaaagac ctacaggaaa actactgtcg aaatcctcga	1380
ggggaagaag ggggaccctg gtgtttcaca agcaatccag aggtacgcta cgaagtctgt	1440 1500
gacatteete agtgtteaga agttgaatge atgacetgea atggggagag ttategaggt	1560
ctcatggatc atacagaatc aggcaagatt tgtcagcgct gggatcatca gacaccacac cggcacaaat tcttgcctga aagatatccc gacaagggct ttgatgataa ttattgccgc	1620
aatcccgatg gccagccgag gccatggtgc tatactcttg accctcacac ccgctgggag	1680
tactgtgcaa ttaaaacatg cgctgacaaa gctgacgacg acgacaaaca ccaccaccac	1740
caccaccact agggtcgac	1759



